



SEQUENCE LISTING

(1) GENERAL INFORMATION

- 70000
- (i) APPLICANT: Ullrich,, Axel
Gishizsky,, Mikhail
Sures,, Irman G.
- (ii) TITLE OF THE INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TYROSINE KINASES
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York,
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: PatentIn, Ver 1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/426,509
(B) FILING DATE: 21-APR-1995
(C) CLASSIFICATION:
- e' (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/232,545
(B) FILING DATE: 22-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Coruzzi, Laura A
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7683-0074-999
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-790-9090
(B) TELEFAX: 212-869-9741
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGCTCCAA	GTTGTGCAGC	CGGGACCGCC	TCGGGGTGTG	CAGCCGGCTC	GCGGAGGCCC	60
TCCTGGGGGC	GGGCGCGGGG	CGGCTCGGGG	GCGCCCCCTG	AGCAGAAAAC	AGGAAGAACC	120
AGGCTCGGTC	CAGTGGCACC	CAGCTCCCTA	CCTCCTGTGC	CAGCCGCCTG	GCCTGTGGCA	180
GGCCATTCCC	AGCGTCCCCG	ACTGTGACCA	CTTGCTCAGT	GTGCCTCTCA	CCTGCCTCAG	240
TTTCCCTCTG	GGGGGCGATG	GCGGGGCGAG	GCTCTCTGGT	TTCTTGGCGG	GCATTTCACG	300

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GCTGTGATTC	TGCTGAGGAA	CTTCCCCGGG	TGAGCCCCCG	CTTCCTCCGA	GCCTGGCACC	360
CCCCCTCCCGT	CTCAGCCAGG	ATGCCAACGA	GGCGCTGGGC	CCCGGGCACC	CAGTGTATCA	420
CCAAATGCGA	GCACACCCGC	CCCAAGCCAG	GGGAGCTGGC	CTTCCGCAAG	GGCGACGTGG	480
TCACCATCCT	GGAGGCCTGC	GAGAACAAGA	GCTGGTACCG	CGTCAAGCAC	CACACCAAGT	540
GACAGGAGGG	GCTGCTGGCA	GCTGGGGCGC	TGCGGGAGCG	GGAGGCCCTC	TCCGCAGACC	600
CCAAGCTCAG	CCTCATGCCG	TGGTTCCACG	GGAAGATCTC	GGGCCAGGAG	GCTGTCCAGC	660
AGCTGCAGCC	TCCCGAGGAT	GGGCTGTTCC	TGGTGCGGGA	GTCCGCGCGC	CACCCCGGCG	720
ACTACGTCCCT	GTGCGTGAGC	TTTGGCCGCG	ACGTCATCCA	CTACCGCGTG	CTGCACCGCG	780
ACGGCCACCT	CACAATCGAT	GAGGCCGTGT	TCTTCTGCAA	CCTCATGGAC	ATGGTGGAGC	840
ATTACAGCAA	GGACAAGGGC	GCTATCTGCA	CCAAGCTGGT	GAGACCAAAG	CGGAAACACG	900
GGACCAAGTC	GGCCGAGGAG	GAGCTGGCCA	GGGCGGGCTG	GTTACTGAAC	CTGCAGCATT	960
TGACATTGGG	AGCACAGATC	GGAGAGGGAG	AGTTTGGAGC	TGTCCTGCAG	GGTGAGTACC	1020
TGGGGCAAAA	GGTGGCCGTG	AAGAATATCA	AGTGTGATGT	GACAGCCAG	GCCTTCCTGG	1080
ACGAGACGGC	CGTCATGACG	AAGATGCAAC	ACGAGAACCT	GGTGCGTCTC	CTGGGCGTGA	1140
TCCTGCACCA	GGGGCTGTAC	ATTGTTCATG	AGCACGTGAG	CAAGGGCAAC	CTGGTGAAC	1200
TTCTGCGGAC	CCGGGGTCGA	GCCCTCGTGA	ACACCGCTCA	GCTCCTGCAG	TTTTCTCTGC	1260
ACGTGGCCGA	GGGCATGGAG	TACCTGGAGA	GCAAGAAGCT	TGTGCACCGC	GACCTGGCCG	1320
CCCGCAACAT	CCTGGTCTCA	GAGGACCTGG	TGGCCAAGGT	CAGCGACTTT	GGCCTGGCCA	1380
AAGCCGAGCG	GAAGGGGCTA	GACTCAAGCC	GGCTGCCCGT	CAAGTGGACG	GCGCCCGAGG	1440
CTCTCAAACA	CGGGAAGTTC	ACCAGCAAGT	CGGATGTCTG	GAGTTTTGGG	GTGCTGCTCT	1500
GGGAGGTCTT	CTCATATGGA	CGGGCTCCGT	ACCCTAAAAT	GTCCTGAAA	GAGGTGTCGG	1560
AGGCCGTGGA	GAAGGGGTAC	CGCATGGAAC	CCCCCGAGGG	CTGTCCAGGC	CCCGTGCACG	1620
TCCTCATGAG	CAGCTGCTGG	GAGGCAGAGC	CCGCCCCGCC	GCCACCCTTC	CGCAAACCTG	1680
CCGAGAAGCT	GGCCCGGGAG	CTACGCAGTG	CAGGTGCCCC	AGCCTCCGTC	TCAGGGCAGG	1740
ACGCCGACGG	CTCCACCTCG	CCCCGAAGCC	AGGAGCCCTG	ACCCACCCCG	GTGGGGCCCT	1800
TGGCCCCAGA	GGACCGAGAG	AGTGGAGAGT	GCGGCGTGGG	GGCACTGACC	AGGCCCAAGG	1860
AGGGTCCAGG	CGGGCAAGTC	ATCCTCCTGG	TGCCCACAGC	AGGGGCTGGC	CCACGTAGGG	1920
GGCTCTGGGC	GGCCCGTGGA	CACCCACAGC	CTGCGAAGGA	TGATCGCCCC	ATAAAGACGG	1980
ATTCTAAGGA	CTCTAAAAAA					2000

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gly	Arg	Gly	Ser	Leu	Val	Ser	Trp	Arg	Ala	Phe	His	Gly	Cys
1				5					10					15	
Asp	Ser	Ala	Glu	Glu	Leu	Pro	Arg	Val	Ser	Pro	Arg	Phe	Leu	Arg	Ala
		20						25					30		
Trp	His	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala	
		35					40					45			
Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro
	50					55					60				
Gly	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Val	Val	Thr	Ile	Leu	Glu	Ala
65					70					75				80	
Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln
			85						90					95	
Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser
		100						105					110		
Ala	Asp	Pro	Lys	Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Ser
		115					120					125			
Gly	Gln	Glu	Ala	Val	Gln	Gln	Leu	Gln	Pro	Pro	Glu	Asp	Gly	Leu	Phe
	130					135					140				
Leu	Val	Arg	Glu	Ser	Ala	Arg	His	Pro	Gly	Asp	Tyr	Val	Leu	Cys	Val
145					150					155				160	
Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly
			165						170					175	
His	Leu	Thr	Ile	Asp	Glu	Ala	Val	Phe	Phe	Cys	Asn	Leu	Met	Asp	Met
		180						185					190		
Val	Glu	His	Tyr	Ser	Lys	Asp	Lys	Gly	Ala	Ile	Cys	Thr	Lys	Leu	Val

195 200 205
 Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
 210 215 220
 Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
 225 230 235 240
 Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
 245 250 255
 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
 260 265 270
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
 275 280 285
 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
 290 295 300
 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
 305 310 315 320
 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
 325 330 335
 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
 340 345 350
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
 355 360 365
 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
 370 375 380
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
 385 390 395 400
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
 405 410 415
 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
 420 425 430
 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
 435 440 445
 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
 450 455 460
 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
 465 470 475 480
 Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala
 485 490 495
 Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
 500 505

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTTTTGT	CTTAGAGCTT	GAGAGTCAAA	GTTAAGGACC	CACATGTATA	CTTCGGCTCT	60
AGCGAGTCTA	AGGATGATAA	TATGGATACA	AAATCTATT	TAGAAGAACT	TCTTCTCAAA	120
AGATCACAGC	AAAAGAAGAA	AATGTCACCA	AATAATTACA	AAGAACGGCT	TTTTGTTTTG	180
ACCAAAACAA	ACCTTTCCTA	CTATGAATAT	GACAAAATGA	AAAGGGGCAG	CAGAAAAGGA	240
TCCATTGAAA	TTAAGAAAT	CAGATGTGTG	GAGAAAGTAA	ATCTCGAGGA	GCAGACGCCT	300
GTAGAGAGAC	AGTACCCATT	TCAGATTGTC	TATAAAGATG	GGCTTCTCTA	TGTCTATGCA	360
TCAAATGAAG	AGAGCCGAAG	TCAGTGGTTG	AAAGCATTAC	AAAAAGAGAT	AAGGGGTAAC	420
CCCCACCTGC	TGGTCAAGTA	CCATAGTGGG	TTCTTCGTGG	ACGGGAAGTT	CCTGTGTTGC	480
CAGCAGAGCT	GTAAAGCAGC	CCCAGGATGT	ACCCTCTGGG	AAGCATATGC	TAATCTGCAT	540
ACTGCAGTCA	ATGAAGAGAA	ACACAGAGTT	CCCACCTTCC	CAGACAGAGT	GCTGAAGATA	600
CCTCGGGCAG	TTCTTGTTC	CAAAATGGAT	GCACCATCTT	CAAGTACCAC	TCTAGCCCCA	660
TATGACAACG	AATCAAAGAA	AAACTATGGC	TCCAGCCAC	CATCTTCAAG	TACCAGTCTA	720
GCGCAATATG	ACAGCAACTC	AAAGAAAATC	TATGGCTCCC	AGCCAAACTT	CAACATGCAG	780
TATATTCCAA	GGGAAGACTT	CCCTGACTGG	TGGCAAGTAA	GAAAAGTAA	AAGTAGCAGC	840
AGCAGTGAAG	ATGTTGCAAG	CAGTAACCAA	AAAGAAAGAA	ATGTGAATCA	CACCACCTCA	900
AAGATTTCAT	GGGAATTCCC	TGAGTCAAGT	TCATCTGAAG	AAGAGGAAAA	CCTGGATGAT	960

TATGACTGGT	TTGCTGGTAA	CATCTCCAGA	TCACAATCTG	AACAGTTACT	CAGACAAAAG	1020
GGAAAAGAAG	GAGCATTTAT	GGTTAGAAAT	TCGAGCCAAG	TGGGAATGTA	CACAGTGTCC	1080
TTATTTAGTA	AGGCTGTGAA	TGATAAAAAA	GGAAGTGTCA	AACATTACCA	CGTGCAATCA	1140
AATGCTGAGA	ACAAATTATA	CCTGGCAGAA	AACTACTGTT	TTGATTCCAT	TCCAAAGCTT	1200
ATTCATTATC	ATCAACACAA	TTCAGCAGGC	ATGATCACAC	GGCTCCGCCA	CCCTGTGTCA	1260
ACAAAGGCCA	ACAAGGTCCC	CGACTCTGTG	TCCCTGGGAA	ATGGAATCTG	GGAAGTGAAG	1320
AGAGAAGAGA	TTACCTTGTT	GAAGGAGCTG	GGAAGTGGCC	AGTTTGGAGT	GGTCCAGCTG	1380
GGCAAGTGGA	AGGGGCAGTA	TGATGTTGCT	GTTAAGATGA	TCAAGGAGGG	CTCCATGTCA	1440
GAAGATGAAT	TCTTTCAGGA	GGCCCAGACT	ATGATGAAAC	TCAGCCATCC	CAAGCTGGTT	1500
AAATTCATATG	GAGTGTGTTT	AAAGGAATAC	CCCATATACA	TAGTGACTGA	ATATATAAGC	1560
AATGGCTGCT	TGCTGAATTA	CCTGAGGAGT	CACGGAAAAG	GAAGTGAACC	TTCCAGCTCT	1620
TTAGAAATGT	GCTACGATGT	CTGTGAAGGC	ATGGCCTTCT	TGGAGAGTCA	CCAATTCATA	1680
CACCGGGACT	TGGCTGCTCG	TAAGTGTCTG	GTGGACAGAG	ATCTCTGTGT	GAAAGTATCT	1740
GACTTTGGAA	TGACAAGGTA	TGTTCTTGAT	GACCATATAG	TCAGTTCAGT	CGGAACAAAG	1800
TTTCCAGTCA	AGTGGTCAGC	TCCAGAGGTG	TTTCATTACT	TCAAATACAG	CAGCAAGTCA	1860
GACGTATGGG	CATTTGGGAT	CCTGATGTGG	GAGGTGTTCA	GCCTGGGGAA	GCAGCCCTAT	1920
GACTTGTATG	ACAAGTCCCA	GGTGGTCTTG	AAGGTCTCCC	AGGGCCACAG	GCTTTACCGG	1980
CCCCACCTGG	CATCGGACAC	CATCTACCAG	ATCATGTACA	GCTGCTGGCA	CGAGCTTCCA	2040
GAAAAGCGTC	CCACATTTCA	GCAACTCCTG	TCTTCCATTG	AACCACTTCG	GGAAAAAGAC	2100
AAGCATTGAA	GAAGAAATTA	GGAGTGCTGA	TAAGAATGAA	TATAGATGCT	GGCCAGCATT	2160
TTCATTCAAT	TTAAGGAAAG	TAGCAAGGCA	TAATGTAATT	TAGCTAGTTT	TTAATAGTGT	2220
TCTCTGTATT	GTCTATTATT	TAGAAATGAA	CAAGGCAGGA	AACAAAAGAT	TCCCTTGAAA	2280
TTTAGGTCAA	ATTAGTAATT	TTGTTTATGC	TGCCCCGTAT	ATAACACTTT	CCAGCCTATA	2340
GCAGAAGCAC	ATTTTCAGAC	TGCAATATAG	AGACTGTGTT	CATGTGTAAA	GACTGAGCAG	2400
AACTGAAAAA	TTACTTATTG	GATATTCATT	CTTTTCTTTA	TATTGTCATT	GTCACAACAA	2460
TTAAATATAC	TACCAAGTAC	AAAAAATAAA	AAAAAATAAA			2500

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Thr Lys Ser Ile Leu Glu Glu Leu Leu Leu Lys Arg Ser Gln
1 5 10 15
Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr Lys Glu Arg Leu Phe Val
20 25 30
Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu Tyr Asp Lys Met Lys Arg
35 40 45
Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
50 55 60
Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
65 70 75 80
Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
85 90 95
Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly
100 105 110
Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
115 120 125
Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr
130 135 140
Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys
145 150 155 160
His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
165 170 175
Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala
180 185 190
Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser
195 200 205
Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr
210 215 220

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Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
 225 230 235 240
 Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Ser Glu
 245 250 255
 Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
 260 265 270
 Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Ser Glu Glu Glu
 275 280 285
 Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser
 290 295 300
 Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met
 305 310 315 320
 Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
 325 330 335
 Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
 340 345 350
 Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
 355 360 365
 Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
 370 375 380
 Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro
 385 390 395 400
 Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
 405 410 415
 Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
 420 425 430
 Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys
 435 440 445
 Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met
 450 455 460
 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
 465 470 475 480
 Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
 485 490 495
 Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
 500 505 510
 Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
 515 520 525
 Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
 530 535 540
 Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr
 545 550 555 560
 Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
 565 570 575
 Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
 580 585 590
 Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
 595 600 605
 Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
 610 615 620
 Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
 625 630 635 640
 Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
 645 650 655
 Pro Thr Phe Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys
 660 665 670
 Asp Lys His
 675

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

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cont.

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGACTGGT	CGAAAGACAG	GAACAGACTT	GAAACAGGGG	GAGAGCTCCT	GGCGAAACGA	60
AGACGTGGAG	GTTTTACCAG	GGATAAGAA	AAAAGACACC	TTCCTAGTGA	GCAGCTGCCC	120
AGCTCCTGCT	CAGTTTTGCC	TCGGGGTAGC	ACCTCCAGCC	ACAGAAAGCA	AGCCGGTAAG	180
TCTCTCCAGG	TAGGACTTGC	TGCAACCCAG	CTGCTGGACT	GATCTGAAAC	GGGACTTTGC	240
ATACTCTCCG	AAGTATGGTG	AGTTGGTGCT	GACTTCAAAG	TTGCCTGGTG	AAGGAAGATA	300
AGGTGGATCG	CAGAGACTAA	GGGGAGAGGG	AGAAGCCCTG	CTCCTCTTCT	CCCCACCAAG	360
GCACAATGAG	CAACATCTGT	CAGAGGCTCT	GGGAGTACCT	AGAACCCTAT	CTCCCCTGTT	420
TGTCCACGGA	GGCAGACAAG	TCAACCGTGA	TTGAAAATCC	AGGGGCCCTT	TGCTCTCCCC	480
AGTCACAGAG	GCATGGCCAC	TACTTTGTGG	CTTTGTTTTGA	TTACCAGGCT	CGGACTGCTG	540
AGGACTTGAG	CTTCCGAGCA	GGTGACAAAC	TTCAAGTTCT	GGACACTTTG	CATGAGGGCT	600
GGTGGTTTGC	CAGACACTTG	GAGAAAAGAC	GAGATGGCTC	CAGTCAGCAA	CTACAAGGCT	660
ATATTCCCTC	TAACTACGTG	GCTGAGGACA	GAAGCCTACA	GGCAGAGCCG	TGGTTCTTTG	720
GAGCAATCGG	AAGATCAGAT	GCAGAGAAAC	AACTATTATA	TTCAGAAAAC	AAGACCGGTT	780
CCTTTCTAAT	CAGAGAAAGT	GAAAGCCAAA	AAGGAGAATT	CTCTCTTTCA	GTTTTAGATG	840
GAGCAGTTGT	AAAACACTAC	AGAATTAAAA	GACTGGATGA	AGGGGGATTT	TTTCTCACGC	900
GAAGAAGAAT	CTTTTCAACA	CTGAACGAAT	TTGTGAGCCA	CTACACCAAG	ACAAGTGACG	960
GCCTGTGTGT	CAAGCTGGGG	AAACCATGCT	TAAAGATCCA	GGTCCCAGCT	CCATTTGATT	1020
TGTCGTATAA	AACCGTGGAC	CAATGGGAGA	TAGACCGCAA	CTCCATACAG	CTTCTGAAGC	1080
GATTGGGATC	TGGTCAGTTT	GGCGAAGTAT	GGGAAGGTCT	GTGGAACAAT	ACCACTCCAG	1140
TAGCAGTGAA	AACATTAAAA	CCAGGTTCAA	TGGATCCAAA	TGACTTCCTG	AGGGAGGCAC	1200
AGATAATGAA	GAACCTAAGA	CATCCAAAGC	TTATCCAGCT	TTATGCTGTT	TGCACTTTAG	1260
AAGATCCAAT	TTATATTATT	ACAGAGTTGA	TGAGACATGG	AAGTCTGCAA	GAATATCTCC	1320
AAAATGACAC	TGGATCAAAA	ATCCATCTGA	CTCAACAGGT	AGACATGGCG	GCACAGGTTG	1380
CCTCTGGAAT	GGCCTATCTG	GAGTCTCGGA	ACTACATTCA	CAGAGATCTG	GCTGCCAGAA	1440
ATGTCCTCGT	TGGTGAACAT	AATATCTACA	AAGTAGCAGA	TTTTGGACTT	GCCAGAGTTT	1500
TTAAGGTAGA	TAATGAAGAC	ATCTATGAAT	CTAGACACGA	AATAAAGCTG	CCGGTGAAGT	1560
GGATGCGGCC	CGAAGCCATT	CGTAGTAATA	AATTCAGCAT	TAAGTCCGAT	GTATGGTCAT	1620
TTGGAATCCT	TCTTTATGAA	ATCATTACTT	ATGGCAAAAT	GCCTTACAGT	GGTATGACAG	1680
GTGCCCAGGT	AATCCAGATG	TTGGCTCAAA	ACTATAGACT	TCCGCAACCA	TCCAACGTCT	1740
CACAGCAATT	TTACAACATC	ATGTTGGAGT	GCTGGAATGC	AGAGCCTAAG	GAACGACCTA	1800
CATTTGAGAC	ACTGCGTTGG	AAACTTGAAG	ACTATTTTGA	AACAGACTCT	TCATATTTCAG	1860
ATGCAAAATA	CTTCATAAGA	TGAACACTGG	AGAAGAATAT	CAAATAATAA	AGTAGCAAAA	1920
CAAATTCAAA	TAATCCATTG	CAAAATACAA	TGTTATCAAC	CAACTGCACA	ATCAGTTTAT	1980
CCTGACATAT	TCAAGTGATA	GGATAAAGTT	GGCCATGTAT	TATGAAAAAG	ATTATTTGTG	2040
CATTTTATTG	ACTGGGCAAC	ACTGCAGGAC	AGTCAAGGTC	ATATATAATT	GCTCACTGCC	2100
TGGAAAAATTA	AGCACACTAA	ACCAAGTTAT	TTTTCTTTTT	AAGAGATACT	TACATTTCCA	2160
TTTATTGTTT	GAAATGTCGC	GATCAAGAGA	ATCAACAGAT	GATAGTCCAA	TTTTTACTCA	2220
GTGATGACTG	TGTAGCATTG	TCCTGTTTAC	TGATTAGAGT	GGTTATTTCAT	TATTCCTCAG	2280
ATTGCTGAAT	CCCATCAGGC	TGTTATTATG	AAGGAATTTG	ATTGCTTTGC	TGCACAGCAG	2340
GACCTGTGCT	TTGAGATTTT	TTTTTCTCTT	TTAAAATATC	CTGTAACCTA	AATGATGGTA	2400
AAGCCATGTT	AAATGACTTG	ATTGTACTTG	GAGTAATTGC	ACATTTTTTTT	TATGCATATA	2460
AAAAATGATG	CAGCTGTTGA	GAAAACGAAG	TCTTTTTTCAT	TTTGCAGAAG	GAAATGATGG	2520
AATTTTCTG	TACTTCAGTA	TGTGTCAACT	GAGAGTCATA	TACATTAGTT	TTAATCTCTT	2580
AATATTGAGA	ATCAGGTTGC	AAAACGGATG	AGTTATTATC	TATGGAAATG	TGAGAAATGT	2640
CTAATAGCCC	ATAAAGTCTG	AGAAATAGGT	ATCAAAATAG	TTTAGGAAAA	TGAGAGGAGA	2700
ACAGTAGGAT	TGCTGTGGCC	TAGACTTCTG	AGTAATTAAT	AAAGAAAAAG	AAGTACCAAA	2760
AAAAAAAAAA						2770

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Asn	Ile	Cys	Gln	Arg	Leu	Trp	Glu	Tyr	Leu	Glu	Pro	Tyr	Leu
1				5				10						15	
Pro	Cys	Leu	Ser	Thr	Glu	Ala	Asp	Lys	Ser	Thr	Val	Ile	Glu	Asn	Pro
		20						25					30		
Gly	Ala	Leu	Cys	Ser	Pro	Gln	Ser	Gln	Arg	His	Gly	His	Tyr	Phe	Val

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
1 5 10 15
Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
20 25 30
Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
35 40 45
Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
50 55 60
Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65 70 75 80
Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
85 90 95
Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
100 105 110
Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
115 120 125
Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
130 135 140
Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145 150 155 160
Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
165 170 175
Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
180 185 190
Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
195 200 205
Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210 215 220
Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225 230 235 240
Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
245 250 255
Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
260 265 270
Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
275 280 285
Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
290 295 300
Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
305 310 315 320
Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
325 330 335
Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
340 345 350
Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
355 360 365
Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
370 375 380
Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
385 390 395 400
Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
405 410 415
Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
420 425 430
Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
435 440 445
His Leu
450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 amino acids

63

C

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
1 5 10 15
Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
20 25 30
Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
35 40 45
Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
50 55 60
Glu Thr Val Val Pro Glu Lys Asn Pro Pro Glu Arg Gln Ile Pro
65 70 75 80
Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
85 90 95
Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
100 105 110
Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
115 120 125
Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
130 135 140
Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
145 150 155 160
Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
165 170 175
Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
180 185 190
Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
195 200 205
Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
210 215 220
Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
225 230 235 240
Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
245 250 255
Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
260 265 270
Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
275 280 285
Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
290 295 300
Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
305 310 315 320
Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
325 330 335
Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
340 345 350
Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
355 360 365
Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
370 375 380
Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
385 390 395 400
Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
405 410 415
Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
420 425 430
Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
435 440 445
Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
450 455 460
Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly

C'
cont.

64

C

465		470		475		480									
Cys	Leu	Leu	Asn	Tyr	Leu	Arg	Glu	Met	Arg	His	Arg	Phe	Gln	Thr	Gln
			485						490					495	
Gln	Leu	Leu	Glu	Met	Cys	Lys	Asp	Val	Cys	Glu	Ala	Met	Glu	Tyr	Leu
			500						505					510	
Glu	Ser	Lys	Gln	Phe	Leu	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu
		515					520					525			
Val	Asn	Asp	Gln	Gly	Val	Val	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg
	530					535					540				
Tyr	Val	Leu	Asp	Asp	Glu	Tyr	Thr	Ser	Ser	Val	Gly	Ser	Lys	Phe	Pro
545					550					555					560
Val	Arg	Trp	Ser	Pro	Pro	Glu	Val	Leu	Met	Tyr	Ser	Lys	Phe	Ser	Ser
			565						570					575	
Lys	Ser	Asp	Ile	Trp	Ala	Phe	Gly	Val	Leu	Met	Trp	Glu	Ile	Tyr	Ser
			580					585					590		
Leu	Gly	Lys	Met	Pro	Tyr	Glu	Arg	Phe	Thr	Asn	Ser	Glu	Thr	Ala	Glu
		595					600					605			
His	Ile	Ala	Gln	Gly	Leu	Arg	Leu	Tyr	Arg	Pro	His	Leu	Ala	Ser	Glu
	610					615					620				
Lys	Val	Tyr	Thr	Ile	Met	Tyr	Ser	Cys	Trp	His	Glu	Lys	Ala	Asp	Glu
625					630				635						640
Arg	Pro	Thr	Phe	Lys	Ile	Leu	Leu	Ser	Asn	Ile	Leu	Asp	Val	Met	Asp
				645					650					655	
Glu	Glu	Ser													

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

C' cont.

Met	Asn	Asn	Phe	Ile	Leu	Leu	Glu	Glu	Gln	Leu	Ile	Lys	Lys	Ser	Gln
1				5					10					15	
Gln	Lys	Arg	Arg	Thr	Ser	Pro	Ser	Asn	Phe	Lys	Val	Arg	Phe	Phe	Val
			20					25					30		
Leu	Thr	Lys	Ala	Ser	Leu	Ala	Tyr	Phe	Glu	Asp	Arg	His	Gly	Lys	Lys
		35					40					45			
Arg	Thr	Leu	Lys	Gly	Ser	Ile	Glu	Leu	Ser	Arg	Ile	Lys	Cys	Val	Glu
	50				55						60				
Ile	Val	Lys	Ser	Asp	Ile	Ser	Ile	Pro	Cys	His	Tyr	Lys	Tyr	Pro	Phe
65					70					75					80
Gln	Val	Val	His	Asp	Asn	Tyr	Leu	Leu	Tyr	Val	Phe	Ala	Pro	Asp	Arg
			85						90					95	
Glu	Ser	Arg	Gln	Arg	Trp	Val	Leu	Ala	Leu	Lys	Glu	Glu	Thr	Arg	Asn
			100					105					110		
Asn	Asn	Ser	Leu	Val	Pro	Lys	Tyr	His	Pro	Asn	Phe	Trp	Met	Asp	Gly
		115					120					125			
Lys	Trp	Arg	Cys	Cys	Ser	Gln	Leu	Glu	Lys	Leu	Ala	Thr	Gly	Cys	Ala
	130					135					140				
Gln	Tyr	Asp	Pro	Thr	Lys	Asn	Ala	Ser	Lys	Lys	Pro	Leu	Pro	Pro	Thr
145					150					155					160
Pro	Glu	Asp	Asn	Arg	Arg	Pro	Leu	Trp	Glu	Pro	Glu	Glu	Thr	Val	Val
			165						170					175	
Ile	Ala	Leu	Tyr	Asp	Tyr	Gln	Thr	Asn	Asp	Pro	Gln	Glu	Leu	Ala	Leu
		180					185						190		
Arg	Arg	Asn	Glu	Glu	Tyr	Cys	Leu	Leu	Asp	Ser	Ser	Glu	Ile	His	Trp
		195					200					205			
Trp	Arg	Val	Gln	Asp	Arg	Asn	Gly	His	Glu	Gly	Tyr	Val	Pro	Ser	Ser
	210					215					220				
Tyr	Leu	Val	Glu	Lys	Ser	Pro	Asn	Asn	Leu	Glu	Thr	Tyr	Glu	Trp	Tyr
225					230					235					240

65

C

Asn Lys Ser Ile Ser Arg Asp Lys Ala Glu Lys Leu Leu Leu Asp Thr
 245 250 255
 Gly Lys Glu Gly Ala Phe Met Val Arg Asp Ser Arg Thr Ala Gly Thr
 260 265 270
 Tyr Thr Val Ser Val Phe Thr Lys Ala Val Val Ser Glu Asn Asn Pro
 275 280 285
 Cys Ile Lys His Tyr His Ile Lys Glu Thr Asn Asp Asn Pro Lys Arg
 290 295 300
 Tyr Tyr Val Ala Glu Lys Tyr Val Phe Asp Ser Ile Pro Leu Leu Ile
 305 310 315 320
 Asn Tyr His Gln His Asn Gly Gly Gly Leu Val Thr Arg Leu Arg Tyr
 325 330 335
 Pro Val Cys Phe Gly Arg Gln Lys Ala Pro Val Thr Ala Gly Leu Arg
 340 345 350
 Tyr Gly Lys Trp Val Ile Asp Pro Ser Glu Leu Thr Phe Val Gln Glu
 355 360 365
 Ile Gly Ser Gly Gln Phe Gly Leu Val His Leu Gly Tyr Trp Leu Asn
 370 375 380
 Lys Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly Ala Met Ser Glu
 385 390 395 400
 Glu Asp Phe Ile Glu Glu Ala Glu Val Met Met Lys Leu Ser His Pro
 405 410 415
 Lys Leu Val Gln Leu Tyr Gly Val Cys Leu Glu Gln Ala Pro Ile Cys
 420 425 430
 Leu Val Phe Glu Phe Met Glu His Gly Cys Leu Ser Asp Tyr Leu Arg
 435 440 445
 Thr Gln Arg Gly Leu Phe Ala Glu Thr Leu Leu Gly Met Cys Leu
 450 455 460
 Asp Val Cys Glu Gly Met Ala Tyr Leu Glu Glu Ala Cys Val Ile His
 465 470 475 480
 Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn Gln Val Ile
 485 490 495
 Lys Val Ser Asp Phe Gly Met Thr Arg Phe Val Leu Asp Asp Gln Tyr
 500 505 510
 Thr Ser Ser Thr Gly Thr Lys Phe Pro Val Lys Trp Ala Ser Pro Glu
 515 520 525
 Val Phe Ser Phe Ser Arg Tyr Ser Ser Lys Ser Asp Val Trp Ser Phe
 530 535 540
 Gly Val Leu Met Trp Glu Val Phe Ser Glu Gly Lys Ile Pro Tyr Glu
 545 550 555 560
 Asn Arg Ser Asn Ser Glu Val Val Glu Asp Ile Ser Thr Gly Phe Arg
 565 570 575
 Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
 580 585 590
 His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
 595 600 605
 Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
 610 615 620

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 527 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
 1 5 10 15
 Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
 20 25 30
 Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
 35 40 45

C
 cont.

66

C

Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
 50 55 60
 Tyr Asn Leu Phe Glu Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
 65 70 75 80
 Glu Ile Lys Lys Arg Arg Pro Pro Pro Pro Ile Pro Pro Glu Glu
 85 90 95
 Asn Thr Glu Glu Ile Val Val Ala Met Tyr Asp Phe Gln Ala Thr Glu
 100 105 110
 Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
 115 120 125
 Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
 130 135 140
 Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
 145 150 155 160
 Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
 165 170 175
 Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
 180 185 190
 Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
 195 200 205
 Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
 210 215 220
 Tyr His Lys His Asn Ala Ala Gly Leu Val Thr Arg Leu Arg Tyr Pro
 225 230 235 240
 Val Ser Thr Lys Gly Lys Asn Ala Pro Thr Thr Ala Gly Phe Ser Tyr
 245 250 255
 Asp Lys Trp Glu Ile Asn Pro Ser Glu Leu Thr Phe Met Arg Glu Leu
 260 265 270
 Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln
 275 280 285
 Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu
 290 295 300
 Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys
 305 310 315 320
 Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile
 325 330 335
 Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln
 340 345 350
 Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp
 355 360 365
 Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg
 370 375 380
 Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys
 385 390 395 400
 Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr
 405 410 415
 Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val
 420 425 430
 Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly
 435 440 445
 Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys
 450 455 460
 Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu
 465 470 475 480
 His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg
 485 490 495
 Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu
 500 505 510
 Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg
 515 520 525

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 537 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown

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C

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
1 5 10 15
Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
20 25 30
Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
35 40 45
Asn Tyr Asn Asn Phe His Ala Gly Gly Gln Gly Leu Thr Val Phe
50 55 60
Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
65 70 75 80
Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
85 90 95
Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
100 105 110
Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125
Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
130 135 140
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
145 150 155 160
Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
165 170 175
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
180 185 190
Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
195 200 205
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
210 215 220
Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
225 230 235 240
Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
245 250 255
Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
260 265 270
Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
275 280 285
Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
290 295 300
Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
305 310 315 320
Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
325 330 335
Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
340 345 350
Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
355 360 365
Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
370 375 380
Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
385 390 395 400
Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
405 410 415
Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
420 425 430
Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
435 440 445
Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
450 455 460
Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
465 470 475 480
Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His

C' work

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C

				485					490					495			
Glu	Leu	Met	Ile	His	Cys	Trp	Lys	Lys	Asp	Pro	Glu	Glu	Arg	Pro	Thr		
			500					505					510				
Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu	Glu	Asp	Tyr	Phe	Thr	Ala	Thr	Glu		
		515					520					525					
Pro	Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu									
	530					535											

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

C. conf.

Met	Gly	Cys	Val	His	Cys	Lys	Glu	Lys	Ile	Ser	Gly	Lys	Gly	Gln	Gly		
1				5					10					15			
Gly	Ser	Gly	Thr	Gly	Thr	Pro	Ala	His	Pro	Pro	Ser	Gln	Tyr	Asp	Pro		
			20					25					30				
Asp	Pro	Thr	Gln	Leu	Ser	Gly	Ala	Phe	Thr	His	Ile	Pro	Asp	Phe	Asn		
		35				40					45						
Asn	Phe	His	Ala	Ala	Ala	Val	Ser	Pro	Pro	Val	Pro	Phe	Ser	Gly	Pro		
	50				55					60							
Gly	Phe	Tyr	Pro	Cys	Asn	Thr	Leu	Gln	Ala	His	Ser	Ser	Ile	Thr	Gly		
65				70				75						80			
Gly	Gly	Val	Thr	Leu	Phe	Ile	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr		
			85					90					95				
Glu	Asp	Asp	Leu	Ser	Phe	Gln	Lys	Gly	Glu	Lys	Phe	His	Ile	Ile	Asn		
			100					105					110				
Asn	Thr	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Ala		
	115						120					125					
Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln		
	130					135					140						
Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg		
145					150					155				160			
Gln	Leu	Leu	Cys	His	Gly	Asn	Cys	Arg	Gly	Thr	Phe	Leu	Ile	Arg	Glu		
			165					170					175				
Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp		
			180					185					190				
Glu	Ala	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp		
	195						200					205					
Ser	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Ile	Gln		
	210					215					220						
Gln	Leu	Val	Gln	His	Tyr	Ile	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys	Arg		
225				230					235					240			
Leu	Ala	Val	Pro	Cys	Pro	Lys	Gly	Thr	Pro	Lys	Leu	Ala	Asp	Leu	Ser		
			245						250					255			
Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln	Leu		
			260					265					270				
Leu	Gln	Lys	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr		
	275					280						285					
Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr		
	290				295						300						
Met	Ser	Pro	Glu	Ala	Phe	Leu	Glu	Glu	Ala	Gln	Ile	Met	Lys	Arg	Leu		
305				310					315					320			
Arg	His	Asp	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro		
			325					330					335				
Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser	Gln	Gly	Ser	Leu	Leu	Asp	Phe		
			340				345					350					
Leu	Lys	Asp	Gly	Asp	Gly	Arg	Tyr	Leu	Lys	Leu	Pro	Gln	Leu	Val	Asp		
	355					360					365						
Met	Ala	Ala	Gln	Ile	Ala	Ala	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Met	Asn		

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C

370		375		380
Tyr Ile His Arg Asp	Leu Arg Ala Ala Asn	Ile Leu Val Gly Asp Asn		
385		390		400
Leu Val Cys Lys Ile	Ala Asp Phe Gly Leu	Ala Arg Leu Ile Glu Asp		
	405	410		415
Asn Glu Tyr Thr Ala	Arg Gln Gly Ala Lys	Phe Pro Ile Lys Trp Thr		
	420	425		430
Ala Pro Glu Ala Ala	Leu Phe Gly Lys Phe	Thr Ile Lys Ser Asp Val		
	435	440		445
Trp Ser Phe Gly Ile	Leu Leu Thr Glu Leu	Val Thr Lys Gly Arg Val		
	450	455		460
Pro Tyr Pro Gly Met	Asn Asn Arg Glu Val	Leu Glu Gln Val Glu Arg		
465		470		480
Gly Tyr Arg Met Gln	Cys Pro Gly Gly Cys	Pro Pro Ser Leu His Asp		
	485	490		495
Val Met Val Gln Cys	Trp Lys Arg Glu Pro	Glu Glu Arg Pro Thr Phe		
	500	505		510
Glu Tyr Leu Gln Ser	Phe Leu Glu Asp	Tyr Phe Thr Ala Thr Glu Pro		
	515	520		525
Gln Tyr Gln Pro Gly	Asp Asn Gln			
530		535		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

C' cent.

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg	
1 5 10 15	
Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe	
20 25 30	
Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg	
35 40 45	
Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe	
50 55 60	
Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly	
65 70 75 80	
Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu	
85 90 95	
Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln	
100 105 110	
Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser	
115 120 125	
Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp	
130 135 140	
Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu	
145 150 155 160	
Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu	
165 170 175	
Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser	
180 185 190	
Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg	
195 200 205	
Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn	
210 215 220	
Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu	
225 230 235 240	
Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln	
245 250 255	
Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu	

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C

			260					265					270				
Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr		
		275					280					285					
Trp	Asn	Gly	Thr	Thr	Arg	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly	Thr		
	290					295					300						
Met	Ser	Pro	Glu	Ala	Phe	Leu	Gln	Glu	Ala	Gln	Val	Met	Lys	Lys	Leu		
305					310					315					320		
Arg	His	Glu	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro		
			325						330					335			
Ile	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Ser	Lys	Gly	Ser	Leu	Leu	Asp	Phe		
		340					345						350				
Leu	Lys	Gly	Glu	Thr	Gly	Lys	Tyr	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp		
	355						360					365					
Met	Ala	Ala	Gln	Ile	Ala	Ser	Gly	Met	Ala	Tyr	Val	Glu	Arg	Met	Asn		
370						375					380						
Tyr	Val	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Asn		
385					390					395					400		
Leu	Val	Cys	Lys	Val	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Ile	Glu	Asp		
			405						410					415			
Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr		
			420					425					430				
Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val		
	435						440					445					
Trp	Ser	Phe	Gly	Ile	Leu	Leu	Thr	Glu	Leu	Thr	Thr	Lys	Gly	Arg	Val		
450					455						460						
Pro	Tyr	Pro	Gly	Met	Val	Asn	Arg	Glu	Val	Leu	Asp	Gln	Val	Glu	Arg		
465					470					475					480		
Gly	Tyr	Arg	Met	Pro	Cys	Pro	Pro	Glu	Cys	Pro	Glu	Ser	Leu	His	Asp		
			485						490					495			
Leu	Met	Cys	Gln	Cys	Trp	Arg	Lys	Glu	Pro	Glu	Glu	Arg	Pro	Thr	Phe		
		500						505					510				
Glu	Tyr	Leu	Gln	Ala	Phe	Leu	Glu	Asp	Tyr	Phe	Thr	Ser	Thr	Glu	Pro		
	515						520					525					
Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu										
530						535											

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Cys	Ile	Lys	Ser	Lys	Glu	Asn	Lys	Ser	Pro	Ala	Ile	Lys	Tyr
1			5					10					15		
Arg	Pro	Glu	Asn	Thr	Pro	Glu	Pro	Val	Ser	Thr	Ser	Val	Ser	His	Tyr
		20						25					30		
Gly	Ala	Glu	Pro	Thr	Thr	Val	Ser	Pro	Cys	Pro	Ser	Ser	Ser	Ala	Lys
	35						40					45			
Gly	Thr	Ala	Val	Asn	Phe	Ser	Ser	Leu	Ser	Met	Thr	Pro	Phe	Gly	Gly
	50					55				60					
Ser	Ser	Gly	Val	Thr	Pro	Phe	Gly	Gly	Ala	Ser	Ser	Ser	Phe	Ser	Val
65					70					75				80	
Val	Pro	Ser	Ser	Tyr	Pro	Ala	Gly	Leu	Thr	Gly	Gly	Val	Thr	Ile	Phe
			85					90					95		
Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Thr	Glu	Asp	Leu	Ser	Phe
		100						105					110		
Lys	Lys	Gly	Glu	Arg	Phe	Gln	Ile	Ile	Asn	Asn	Thr	Glu	Gly	Asp	Trp
	115						120					125			
Trp	Glu	Ala	Arg	Ser	Ile	Ala	Thr	Gly	Lys	Asn	Gly	Tyr	Ile	Pro	Ser
	130					135					140				
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe

145 150 155 160
 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175
 Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190
 Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205
 Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220
 Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240
 Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255
 Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270
 Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285
 Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300
 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320
 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335
 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365
 Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala

		35				40				45				
His	Ile	Pro	Asn	Tyr	Ser	Asn	Phe	Ser	Ser	Gln	Ala	Ile	Asn	Pro
50						55					60			Gly
Phe	Leu	Asp	Ser	Gly	Thr	Ile	Arg	Gly	Val	Ser	Gly	Ile	Gly	Val
65					70					75				80
Leu	Phe	Ile	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Glu	Asp	Asp
			85					90					95	Leu
Thr	Phe	Thr	Lys	Gly	Glu	Lys	Phe	His	Ile	Leu	Asn	Asn	Thr	Glu
			100					105				110		Gly
Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Lys	Thr	Gly	Cys
		115					120					125		Ile
Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln	Ala	Glu	Glu
130						135					140			Trp
Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu
145				150						155				160
Pro	Gly	Asn	Pro	Gln	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Thr
				165					170					175
Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Gln	Thr	Arg
		180						185				190		Gly
Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Met	Gly	Gly
		195					200					205		Tyr
Tyr	Ile	Thr	Thr	Arg	Val	Gln	Phe	Asn	Ser	Val	Gln	Glu	Leu	Val
210					215						220			Gln
His	Tyr	Met	Glu	Val	Asn	Asp	Gly	Leu	Cys	Asn	Leu	Leu	Ile	Ala
225					230					235				240
Cys	Thr	Ile	Met	Lys	Pro	Gln	Thr	Leu	Gly	Leu	Ala	Lys	Asp	Ala
			245						250					255
Glu	Ile	Ser	Arg	Ser	Ser	Ile	Thr	Leu	Glu	Arg	Arg	Leu	Gly	Thr
		260						265				270		Gly
Cys	Phe	Gly	Asp	Val	Trp	Leu	Gly	Thr	Trp	Asn	Gly	Ser	Thr	Lys
		275					280				285			Val
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Lys	Ala	Phe
290					295						300			Leu
Glu	Glu	Ala	Gln	Val	Met	Lys	Leu	Leu	Arg	His	Asp	Lys	Leu	Val
305				310						315				Gln
Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu
			325						330					Phe
Met	Cys	His	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Asn	Pro	Glu	Gly
		340						345					350	Gln
Asp	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Val	Ala
		355					360					365		Glu
Gly	Met	Ala	Tyr	Met	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu
370					375						380			Arg
Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Arg	Leu	Ala	Cys	Lys	Ile	Ala
385				390						395				400
Phe	Gly	Leu	Ala	Arg	Leu	Ile	Lys	Asp	Asp	Glu	Tyr	Asn	Pro	Cys
			405						410					Gln
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu
		420						425				430		Phe
Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu
		435					440					445		Leu
Thr	Glu	Leu	Ile	Thr	Lys	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Asn
450					455						460			Lys
Arg	Glu	Val	Leu	Glu	Gln	Val	Glu	Gln	Gly	Tyr	His	Met	Pro	Cys
465				470					475					480
Pro	Gly	Cys	Pro	Ala	Ser	Leu	Tyr	Glu	Ala	Met	Glu	Gln	Thr	Trp
			485						490				495	Arg
Leu	Asp	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe
		500						505				510		Leu
Glu	Asp	Tyr	Phe	Thr	Ser	Ala	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Asp
		515					520					525		Gln
Thr														

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

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G

(A) LENGTH: 512 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
1 5 10 15
Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30
Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
35 40 45
Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
50 55 60
Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
65 70 75 80
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
100 105 110
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125
Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
130 135 140
Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
145 150 155 160
Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175
Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
180 185 190
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
195 200 205
Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
210 215 220
Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
225 230 235 240
Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
245 250 255
Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
260 265 270
Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
275 280 285
Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
290 295 300
Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
305 310 315 320
Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly
325 330 335
Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala
340 345 350
Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu
355 360 365
Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala
370 375 380
Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg
385 390 395 400
Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn
405 410 415
Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
420 425 430
Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr
435 440 445
Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg
450 455 460

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74

C

(A) LENGTH: 505 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

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cent.

385				390				395				400			
Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn	Phe	Gly	Ser	Phe	Thr	Ile	Lys
				405					410					415	
Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Met	Glu	Ile	Val	Thr	Tyr
			420					425					430		
Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Ser	Asn	Pro	Glu	Val	Ile	Arg	Ala
			435				440					445			
Leu	Glu	Arg	Gly	Tyr	Arg	Met	Pro	Arg	Pro	Glu	Asn	Cys	Pro	Glu	Glu
	450					455					460				
Leu	Tyr	Asn	Ile	Met	Met	Arg	Cys	Trp	Lys	Asn	Arg	Pro	Glu	Glu	Arg
465					470					475					480
Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Val	Leu	Asp	Asp	Phe	Tyr	Thr	Ala
				485					490					495	
Thr	Glu	Ser	Gln	Tyr	Gln	Gln	Gln	Pro							
			500					505							

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Gly	Cys	Gly	Cys	Ser	Ser	His	Pro	Glu	Asp	Asp	Trp	Met	Glu	Asn
1				5					10					15	
Ile	Asp	Val	Cys	Glu	Asn	Cys	His	Tyr	Pro	Ile	Val	Pro	Leu	Asp	Gly
			20					25					30		
Lys	Gly	Thr	Leu	Leu	Ile	Arg	Asn	Gly	Ser	Glu	Val	Arg	Asp	Pro	Leu
			35				40					45			
Val	Thr	Tyr	Glu	Gly	Ser	Asn	Pro	Pro	Ala	Ser	Pro	Leu	Gln	Asp	Asn
	50					55					60				
Leu	Val	Ile	Ala	Leu	His	Ser	Tyr	Glu	Pro	Ser	His	Asp	Gly	Asp	Leu
65					70					75				80	
Gly	Phe	Glu	Lys	Gly	Glu	Gln	Leu	Arg	Ile	Leu	Glu	Gln	Ser	Gly	Glu
			85						90					95	
Trp	Trp	Lys	Ala	Gln	Ser	Leu	Thr	Thr	Gly	Gln	Glu	Gly	Phe	Ile	Pro
			100					105					110		
Phe	Asn	Phe	Val	Ala	Lys	Ala	Asn	Ser	Leu	Glu	Pro	Glu	Pro	Trp	Phe
	115						120					125			
Phe	Lys	Asn	Leu	Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro
	130					135					140				
Gly	Asn	Thr	His	Gly	Ser	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Ser	Thr	Ala
145					150					155					160
Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Gln	Asn	Gln	Gly	Glu
			165					170					175		
Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Asn	Leu	Asp	Asn	Gly	Gly	Phe	Tyr
			180					185					190		
Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Gly	Leu	His	Glu	Leu	Val	Arg	His
	195						200						205		
Tyr	Thr	Asn	Ala	Ser	Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ser	Arg	Pro	Cys
	210					215					220				
Gln	Thr	Gln	Lys	Pro	Gln	Lys	Pro	Trp	Trp	Glu	Asp	Glu	Trp	Glu	Val
225					230					235					240
Pro	Arg	Glu	Thr	Leu	Lys	Leu	Val	Glu	Arg	Leu	Gly	Ala	Gly	Gln	Phe
			245						250					255	
Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Gly	His	Thr	Lys	Val	Ala	Val
			260					265					270		
Lys	Ser	Leu	Lys	Gln	Gly	Ser	Met	Ser	Pro	Asp	Ala	Phe	Leu	Ala	Glu
	275						280					285			
Ala	Asn	Leu	Met	Lys	Gln	Leu	Gln	His	Gln	Arg	Leu	Val	Arg	Leu	Tyr
	290					295					300				
Ala	Val	Val	Thr	Gln	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Met	Glu
305					310					315					320

290	Ala	Val	Val	Thr	Gln	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Met	Glu
305	Asn	Gly	Ser	Leu	Val	Asp	Phe	Leu	Lys	Thr	Pro	Ser	Gly	Ile	Lys	Leu
	Thr	Ile	Asn	Lys	Leu	Leu	Asp	Met	Ala	Ala	Gln	Ile	Ala	Glu	Gly	Met
	Ala	Phe	Ile	Glu	Glu	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala
	Asn	Ile	Leu	Val	Ser	Asp	Thr	Leu	Ser	Cys	Lys	Ile	Ala	Asp	Phe	Gly
	Leu	Ala	Arg	Leu	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Glu	Gly	Ala
	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn	Tyr	Gly	Thr
	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Thr	Glu
	Ile	Val	Thr	His	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Thr	Asn	Pro	Glu
	Val	Ile	Gln	Asn	Leu	Glu	Arg	Gly	Tyr	Arg	Met	Val	Arg	Pro	Asp	Asn
	Cys	Pro	Glu	Glu	Leu	Tyr	Gln	Leu	Met	Arg	Leu	Cys	Trp	Lys	Glu	Arg
	Pro	Glu	Asp	Arg	Pro	Thr	Phe	Asp	Tyr	Leu	Arg	Ser	Val	Leu	Glu	Asp
	Phe	Phe	Thr	Ala	Thr	Glu	Gly	Gln	Tyr	Gln	Pro	Gln	Pro			

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Gly	Leu	Leu	Ser	Ser	Lys	Arg	Gln	Val	Ser	Glu	Lys	Gly	Lys	Gly
1				5					10					15	
Trp	Ser	Pro	Val	Lys	Ile	Arg	Thr	Gln	Asp	Lys	Ala	Pro	Pro	Pro	Leu
			20					25					30		
Pro	Pro	Leu	Val	Val	Phe	Asn	His	Leu	Ala	Pro	Pro	Ser	Pro	Asn	Gln
			35			40						45			
Asp	Pro	Asp	Glu	Glu	Glu	Arg	Phe	Val	Val	Ala	Leu	Phe	Asp	Tyr	Ala
			50			55					60				
Ala	Val	Asn	Asp	Arg	Asp	Leu	Gln	Val	Leu	Lys	Gly	Glu	Lys	Leu	Gln
			65			70				75				80	
Val	Leu	Arg	Ser	Thr	Gly	Asp	Trp	Trp	Leu	Ala	Arg	Ser	Leu	Val	Thr
			85						90					95	
Gly	Arg	Glu	Gly	Tyr	Val	Pro	Ser	Asn	Phe	Val	Ala	Pro	Val	Glu	Thr
			100					105					110		
Leu	Glu	Val	Glu	Lys	Trp	Phe	Phe	Arg	Thr	Ile	Ser	Arg	Lys	Asp	Ala
			115				120					125			
Glu	Arg	Gln	Leu	Leu	Ala	Pro	Met	Asn	Lys	Ala	Gly	Ser	Phe	Leu	Ile
			130			135					140				
Arg	Glu	Ser	Glu	Ser	Asn	Lys	Gly	Ala	Phe	Ser	Leu	Ser	Val	Lys	Asp
			145			150				155				160	
Ile	Thr	Thr	Gln	Gly	Glu	Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Ser	Leu
			165					170					175		
Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Thr	Leu
			180					185					190		
Gln	Ala	Leu	Val	Gln	His	Tyr	Ser	Lys	Lys	Gly	Asp	Gly	Leu	Cys	Gln
			195				200				205				
Lys	Leu	Thr	Leu	Pro	Cys	Val	Asn	Leu	Ala	Pro	Lys	Asn	Leu	Trp	Ala

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Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Lys Asn
 245 250 255
 Asn Met Lys Val Ala Ile Lys Thr Leu Lys Glu Gly Thr Met Ser Pro
 260 265 270
 Glu Ala Phe Leu Gly Glu Ala Asn Val Met Lys Thr Leu Gln His Glu
 275 280 285
 Arg Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Pro Ile Tyr Ile
 290 295 300
 Val Thr Glu Tyr Met Ala Arg Gly Cys Leu Leu Asp Phe Leu Lys Thr
 305 310 315 320
 Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg Leu Ile Asp Met Ser Ala
 325 330 335
 Gln Val Ala Glu Gly Met Ala Tyr Ile Glu Arg Met Asn Ser Ile His
 340 345 350
 Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Glu Thr Leu Cys Cys
 355 360 365
 Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Asp Ser Glu Tyr Thr
 370 375 380
 Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala
 385 390 395 400
 Ile His Phe Gly Val Phe Thr Ile Lys Ala Asp Val Trp Ser Phe Gly
 405 410 415
 Val Leu Leu Met Val Ile Val Thr Tyr Gly Arg Val Pro Tyr Pro Gly
 420 425 430
 Met Ser Asn Pro Glu Val Ile Arg Ser Leu Glu His Gly Tyr Arg Met
 435 440 445
 Pro Cys Pro Glu Thr Cys Pro Pro Glu Leu Tyr Asn Asp Ile Ile Thr
 450 455 460
 Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu
 465 470 475 480
 Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu
 485 490 495
 Leu Gln Pro

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATTCCTCA CAGNGACTTN GCNGCNAG

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCTCA ANGTCANAC GTCNGA

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